STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number:	10/559, 434
Source:	PCT10
Date Processed by STIC:	12/16/2005
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THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

1

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 57:-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.2.2 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail. Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in ejectronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

- 1. EFS-Bio (http://www.uspto.gov/efs/downloads/documents.htm, EFS Submission User Manual ePAVE)
- 2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
- 3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05): U.S. Patent and Trademark Office, Mair Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/24/05

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION SERIAL NUMBER: 10/559, 434							
ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE								
1Wrapped Nucleics Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."							
2lnvalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.							
3Misaligned Amino Numbering	The numbering under each 5 th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.							
4Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.							
5Variable Length	Sequence(s)contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.							
6PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.							
7Skipped Sequences (OLD RULES)	Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped							
	Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.							
8Skipped Sequences (NEW RULES)	Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence. <210> sequence id number <400> sequence id number 000							
9Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.							
10Invalid <213> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence							
Use of <220>	Sequence(s)missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)							
PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of Patentln version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.							
13 Misuse of n/Xaa	"n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid							



IFWP

RAW SEQUENCE LISTING DATE: 12/16/2005 TIME: 15:38:57 PATENT APPLICATION: US/10/559,434

Input Set : A:\SEQUENCE LISTING.txt Output Set: N:\CRF4\12162005\J559434.raw

3 <110> APPLICANT: Degussa AG

5 <120> TITLE OF INVENTION: Screening process for hydantoin racemases

7 <130> FILE REFERENCE: 030115 AM

C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/559,434

C--> 10 <141> CURRENT FILING DATE: 2005-12-05

12 <160> NUMBER OF SEQ ID NOS: 16

14 <170> SOFTWARE: PatentIn Ver. 2.1

Does Not Comply Corrected Diskette Needed

ERRORED SEQUENCES

ficial sequence

J2207 golulifier Pls Dissert.

FION: Description of the artificial sequence (1867)

The Asn Pro Asn Ser Ser Ser Ala Leu Thr Glu

Ala Gln Gln Val Val Ala Thr Gly Thr Ile Ile

Ser Arg Gly Pro Ala Val Ile Glu Gly Ser Phe

40

Thr Phe His Leu Ile Glu Glu Val Glu Arg Ala

55

Pro Asp Ala Tyr Val Ile Ala Cys Phe Arg Asp

70

Val Lys Glu Leu Thr Asp Arg Pro Val Val Gly

Ile His Met Ser Ser Phe Val Ala Ala Thr Phe

105

Leu Pro Arg Val Arg Lys His Leu His Glu Leu

120

Ala Thr Asn Arg Leu Ala Ser Ile Lys Leu Pro 156 <210> SEQ ID NO: 157 <211> LENGTH: 237 158 <212> TYPE: PRT 159 <213> ORGANISM: Artificial sequence -> 160 · 160 <223> OTHER INFORMATION: Description of the artificial sequence (1867 162 <400> SEQUENCE: 4 163 Met Arg Ile Leu Val Ile Asn Pro Asn Ser Ser Ser Ala Leu Thr Glu 166 Ser Val Ala Asp Ala Ala Gln Gln Val Val Ala Thr Gly Thr Ile Ile 20 169 Ser Ala Ile Asn Pro Ser Arg Gly Pro Ala Val Ile Glu Gly Ser Phe 35 172 Asp Glu Ala Leu Ala Thr Phe His Leu Ile Glu Glu Val Glu Arg Ala 175 Glu Arg Glu Asn Pro Pro Asp Ala Tyr Val Ile Ala Cys Phe Arg Asp 178 Pro Gly Leu Asp Ala Val Lys Glu Leu Thr Asp Arg Pro Val Val Gly 181 Val Ala Glu Ala Ala Ile His Met Ser Ser Phe Val Ala Ala Thr Phe 182 184 Ser Ile Val Ser Ile Leu Pro Arg Val Arg Lys His Leu His Glu Leu 187 Val Arg Gln Ala Gly Ala Thr Asn Arg Leu Ala Ser Ile Lys Leu Pro 135 140 190 Asn Leu Gly Val Met Ala Phe His Glu Asp Glu His Ala Ala Leu Glu 150 155 193 Thr Leu Lys Gln Ala Ala Lys Glu Ala Val Gln Glu Asp Gly Ala Glu

170

196 Ser Ile Val Leu Gly Cys Ala Gly Met Val Gly Phe Ala Arg Gln Leu

199 Ser Asp Glu Leu Gly Val Pro Val Ile Asp Pro Val Glu Ala Ala Cys

185

165

<210> 1

<211> 6

<212> PRT

<213> Artificial sequence

<220>

<223> Description of the artificial sequence Consensus sequence

Phe Xaa Asp Xaa Gly Leu 5

Pls Explains * 199 localisme which seridue they représents. See Error Explanation en page-6

PYI

of errors shown exist throughout the parce Listing. Please check supposed the sequences for similar errors.

DATE: 12/16/2005

TIME: 15:38:57

```
Input Set : A:\SEQUENCE LISTING.txt
                    Output Set: N:\CRF4\12162005\J559434.raw
                195
                                    200
     200
     202 Arg Val Ala Glu Ser Leu Val Ala Leu Gly Tyr Gln Thr Ser Lys Ala
                                215
     205 Asn Ser Tyr Gln Lys Pro Thr Glu Lys Gln Tyr Leu
E--> 206 225
                            230
    283 <210> SEQ ID NO: 6
                               -> formed 236
    284 <211> LENGTH: 237
     285 <212> TYPE: PRT
     286 <213> ORGANISM: Artificial sequence
     287 <223> OTHER INFORMATION: Description of the artificial sequence (3CH11
E--> 289 <400> SEQUENCE: 6
     290 Met Arg Ile Leu Val Ile Asn Pro Asn Ser Ser Ser Ala Leu Thr Glu
     293 Ser Val Ala Asp Ala Ala Gln Gln Val Val Ala Thr Gly Thr Ile Ile
     296 Ser Ala Ile Asn Pro Ser Arg Gly Pro Ala Val Ile Glu Gly Ser Phe
                35
                                     40
     299 Asp Glu Ala Leu Ala Thr Phe His Leu Ile Glu Glu Val Glu Arg Ala
            50
                                 55
     302 Glu Arg Glu Asn Pro Pro Asp Ala Tyr Val Ile Ala Cys Phe Glu Asp
                             70
                                                 75
     305 Pro Gly Leu Asp Ala Val Lys Glu Leu Thr Asp Arg Pro Val Val Gly
     308 Val Ala Glu Ala Ala Ile His Met Ser Ser Phe Val Ala Ala Thr Phe
    309
                    100
                                         105
                                                             110
     311 Ser Ile Val Ser Ile Leu Pro Arg Val Arg Lys His Leu His Glu Leu
     312
                115
                                    120
     314 Val Arg Gln Ala Gly Ala Thr Asn Arg Leu Ala Ser Ile Lys Leu Pro
                              135
     317 Asn Leu Gly Val Met Ala Phe His Glu Asp Glu His Ala Ala Leu Glu
                            150
                                                155
     320 Thr Leu Lys Gln Ala Ala Lys Glu Ala Val Gln Glu Asp Gly Ala Glu
                         165
                                             170
     323 Ser Ile Val Leu Gly Cys Ala Gly Met Val Gly Phe Ala Arg Gln Leu
                    180
                                        185
     326 Ser Asp Glu Leu Gly Val Pro Val Ile Asp Pro Val Glu Ala Ala Cys
                195
                                    200
     329 Arg Val Ala Glu Ser Leu Val Ala Leu Gly Tyr Gln Thr Ser Lys Ala
                                215
     332 Asn Ser Tyr Gln Lys Pro Thr Glu Lys Gln Tyr Leu
E--> 333 225
                             230
     412 <210> SEQ ID NO: 8
     413 <211> LENGTH: 237
     415 <213> ORGANISM: Artificial sequence 3 P/S Insert 22207
     414 <212> TYPE: PRT
     416 <223> OTHER INFORMATION: Description of the artificial sequence:
     418 <400> SEQUENCE: 8
```

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/559,434

RAW SEQUENCE LISTING DATE: 12/16/2005
PATENT APPLICATION: US/10/559,434 TIME: 15:38:57

Input Set : A:\SEQUENCE LISTING.txt
Output Set: N:\CRF4\12162005\J559434.raw

```
419 Met Arg Ile Leu Val Ile Asn Pro Asn Ser Ser Ser Ala Leu Thr Glu
     422 Ser Val Ala Asp Ala Ala Gln Gln Val Val Ala Thr Gly Thr Ile Ile
     425 Ser Ala Ile Asn Pro Ser Arg Gly Pro Ala Val Ile Glu Gly Ser Phe
                                     40
     428 Asp Glu Ala Leu Ala Thr Phe His Leu Ile Glu Glu Val Glu Arg Ala
             50
                                 55
     431 Glu Arg Glu Asn Pro Pro Asp Ala Tyr Val Ile Ala Cys Phe Gln Asp
                             70
     434 Pro Gly Leu Asp Ala Val Lys Glu Leu Thr Asp Arg Pro Val Val Gly
     437 Val Ala Glu Ala Ala Ile His Met Ser Ser Phe Val Ala Ala Thr Phe
                    100
                                        105
     440 Ser Ile Val Ser Ile Leu Pro Arg Val Arg Lys His Leu His Glu Leu
                                    120
     443 Val Arg Gln Ala Gly Ala Thr Asn Arg Leu Ala Ser Ile Lys Leu Pro
                                135
                                                    140
     446 Asn Leu Gly Val Met Ala Phe His Glu Asp Glu His Ala Ala Leu Glu
     447 145
                            150
                                                155
     449 Thr Leu Lys Gln Ala Ala Lys Glu Ala Val Gln Glu Asp Gly Ala Glu
                                            170
                        165
     452 Ser Ile Val Leu Gly Cys Ala Gly Met Val Gly Phe Ala Arg Gln Leu
                                        185
     455 Ser Asp Glu Leu Gly Val Pro Val Ile Asp Pro Val Glu Ala Ala Cys
                195
                                    200
     458 Arg Val Ala Glu Ser Leu Val Ala Leu Gly Tyr Gln Thr Ser Lys Ala
     459
                                215
     461 Asn Ser Tyr Gln Lys Pro Thr Glu Lys Gln Tyr Leu
E--> 462 225
                            230
     541 <210> SEQ ID NO: 10
                             -> found 236
     542 <211> LENGTH: (237)
     543 <212> TYPE: PRT
                                                 < 2207 Insert
     544 <213> ORGANISM: Artificial sequence
  -> 545 ....
     545 <223> OTHER INFORMATION: Description of the artificial sequence BBS
                                                                            Some Earor
E--> 547 <400> SEQUENCE: 10
     548 Met Arg Ile Leu Val Ile Asn Pro Asn Ser Ser Ser Ala Leu Thr Glu
     551 Ser Val Ala Asp Ala Ala Gln Gln Val Val Ala Thr Gly Thr Ile Ile
                     20
                                         25
     554 Ser Ala Ile Asn Pro Ser Arg Gly Pro Ala Val Ile Glu Gly Ser Phe
     557 Asp Glu Ala Leu Ala Thr Phe His Leu Ile Glu Glu Val Glu Arg Ala
                                 55
     560 Glu Arg Glu Asn Pro Pro Asp Ala Tyr Val Ile Ala Cys Phe Leu Asp
                             70
    563 Pro Gly Leu Asp Ala Val Lys Glu Leu Thr Asp Arg Pro Val Val Gly
                         85
                                             90
```

Conce Listing Please check subsequent sequences for similar errors.

RAW SEQUENCE LISTING DATE: 12/16/2005
PATENT APPLICATION: US/10/559,434 TIME: 15:38:57

Input Set : A:\SEQUENCE LISTING.txt
Output Set: N:\CRF4\12162005\J559434.raw

	566 567	Val	Ala	Glu	Ala 100	Ala	Ile	His	Met	Ser 105	Ser	Phe	Val	Ala	Ala 110	Thr	Phe
	569 570	Ser	Ile	Val 115	Ser	Ile	Leu	Pro	Arg 120	Val	Arg	Lys	His	Leu 125	His	Glu	Leu
		Val	Arg		Ala	Gly	Ala	Thr 135	Asn	Arg	Leu	Ala	Ser 140		Lys	Leu	Pro
	575	Asn 145		Gly	Val	Met	Ala 150		His	Glu	Asp	Glu 155		Ala	Ala	Leu	Glu 160
			Leu	Lys	Gln	Ala 165	Ala	Lys	Glu	Ala	Val 170	Gln	Glu	Asp	Gly	Ala 175	Glu
		Ser	Ile	Val	Leu 180	Gly	Cys	Ala	Gly	Met 185	Val	Gly	Phe	Ala	Arg 190	Gln	Leu
		Ser	Asp	Glu 195	Leu	Gly	Val	Pro	Val 200	Ile	Asp	Pro	Val	Glu 205	Ala	Ala	Cys
	587 588	Arg	Val 210	Ala	Glu	Ser	Leu	Val 215	Ala	Leu	Gly	Tyr	Gln 220	Thr	Ser	Lys	Ala
E>			Ser	Tyr	Gln	Lys	Pro 230	Thr	Glu	Lys	Gln	Tyr 235	Leu				

VARIABLE LOCATION SUMMARY

PATENT APPLICATION: US/10/559,434

DATE: 12/16/2005 TIME: 15:38:58

Input Set : A:\SEQUENCE LISTING.txt

Output Set: N:\CRF4\12162005\J559434.raw

Server Explanation

Use of n's or Xaa's (NEW RULES):

Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
in <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

Seq#:1; Xaa Pos. 2,4
Seq#:14; N Pos. 49

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/559,434 TIME: 15:38:58

DATE: 12/16/2005

Input Set : A:\SEQUENCE LISTING.txt
Output Set: N:\CRF4\12162005\J559434.raw

L:9 M:270 C: Current Application Number differs, Replaced Application Number L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date L:26 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:1 L:26 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:1 L:26 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:0 L:160 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:4 L:162 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:4 L:206 M:252 E: No. of Seq. differs, <211> LENGTH:Input:237 Found:236 SEQ:4 L:287 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:6 L:289 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:6 L:333 M:252 E: No. of Seq. differs, <211> LENGTH:Input:237 Found:236 SEQ:6 L:416 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:8 L:418 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:8 L:462 M:252 E: No. of Seq. differs, <211> LENGTH:Input:237 Found:236 SEQ:8 L:545 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:10 L:547 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:10 L:592 M:252 E: No. of Seq. differs, <211> LENGTH:Input:237 Found:236 SEQ:10 L:832 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:14 L:832 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:14 L:832 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14 after pos.:0